



RAW SEQUENCE LISTING ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 09/810, 861 A

Source: OIPE

Date Processed by STIC: 7/5/2001

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THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,**
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY**

FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.

PATENTIN 2.1 e-mail help: patin21help@uspto.gov or phone 703-306-4119 (R. Wax)

PATENTIN 3.0 e-mail help: patin3help@uspto.gov or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 3.0 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW:

Checker Version 3.0

The Checker Version 3.0 application is a state-of-the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§1.821 - 1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST.25.

Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-compliant. Checker allows public users to check sequence listings in Computer Readable form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO). Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money.

Checker Version 3.0 can be down loaded from the USPTO website at the following address:

<http://www.uspto.gov/web/offices/pac/checker>

OIKE

RAW SEQUENCE LISTING

DATE: 07/05/2001

PATENT APPLICATION: US/09/810,861A

TIME: 10:31:39

Input Set : A:\PTO.txt

Output Set: N:\CRF3\07052001\I810861A.raw

Does Not Comply
Corrected Diskette Needed

see page 5

3 <110> APPLICANT: Mor, Tsafirir
 4 Hermona, Soreq
 5 Charles, Arntzen
 6 Hugh, Mason
 8 <120> TITLE OF INVENTION: EXPRESSION OF RECOMBINANT HUMAN ACETYLCHOLINESTERASE IN
 TRANSGENIC

9 TOMATOES
 11 <130> FILE REFERENCE: BTI-45
 13 <140> CURRENT APPLICATION NUMBER: 09/810,861A
 C--> 14 <141> CURRENT FILING DATE: 2001-06-18
 16 <150> PRIOR APPLICATION NUMBER: 06/190,440
 17 <151> PRIOR FILING DATE: 2000-03-17
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 42 <211> LENGTH: 5767
 43 <212> TYPE: DNA
 44 <213> ORGANISM: synthetic construct
 46 <400> SEQUENCE: 3

29
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 one of the following 3 choices: Scientific
 name, i.e. Genus/species, Unknown or Artificial
 Sequence. In addition the "Unknown or Artificial
 Sequence" organisms shall be ³¹ further described
 in the <220> to <223> feature section.
 see item 10 on ERROR Summary sheet.

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TIME: 10:31:39

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249 <222> LOCATION: (11862)..(12157)

250 <223> OTHER INFORMATION: Identity of sequence residues 11862 to 12157 is unknown.

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388 aatcaggggg taacgcagga aagaacatgt gagcaaaagg ccagcaaaag gccaggaacc 4080
390 gtaaaaaggc cgcgttgctg gcgtttttcc ataggctccg cccccctgac gagcatcaca 4140
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464 atcaatatat ctatagaatg ggcaaagcat aaaaacttgc atggactaat gcttgaaacc 6360
466 caggacaata accttatagc ttgtaaattc tatcataatt gggtaatgac tccaacttat 6420

```

FJL:

Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

VERIFICATION SUMMARY

PATENT APPLICATION: US/09/810,861A

DATE: 07/05/2001

TIME: 10:31:40

Input Set : A:\PTO.txt

Output Set: N:\CRF3\07052001\I810861A.raw

L:14 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:648 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:4
L:650 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:4
L:652 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:4
L:654 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:4
L:656 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:4
L:658 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:4

Raw Sequence Listing Error Summary

ERROR DETECTED

SUGGESTED CORRECTION

SERIAL NUMBER: 09/810,861A

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

- 1 Wrapped Nucleics
 Wrapped Aminos The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor **after** creating it. Please adjust your right margin to .3; this will prevent "wrapping."

- 2 Invalid Line Length The rules require that a line **not exceed** 72 characters in length. This includes white spaces.

- 3 Misaligned Amino
 Numbering The numbering under each 5th amino acid is misaligned. Do **not** use tab codes between numbers; use **space characters**, instead.

- 4 Non-ASCII The submitted file was **not** saved in ASCII(DOS) text, as **required** by the Sequence Rules. Please **ensure your subsequent submission is saved in ASCII text**.

- 5 Variable Length Sequence(s) contain n's or Xaa's representing more than one residue. **Per Sequence Rules, each n or Xaa can only represent a single residue.** Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.

- 6 PatentIn 2.0
 "bug" A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s) . Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. **This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.**

- 7 Skipped Sequences
 (OLD RULES) Sequence(s) missing. If intentional, please insert the following lines for each skipped sequence:
 (2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
 (i) SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)
 (xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
 This sequence is intentionally skipped

 Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.

- 8 Skipped Sequences
 (NEW RULES) Sequence(s) missing. If intentional, please insert the following lines for each skipped sequence.
 <210> sequence id number
 <400> sequence id number
 000

- 9 Use of n's or Xaa's
 (NEW RULES) Use of n's and/or Xaa's have been detected in the Sequence Listing.
 Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present.
 In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.

- 10 ✓ Invalid <213>
 Response Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is **required** when <213> response is Unknown or is Artificial Sequence

- 11 Use of <220> Sequence(s) missing the <220> "Feature" and associated numeric identifiers and responses.
 Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section.
 (See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)

- 12 PatentIn 2.0
 "bug" Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.